

**STIC-Biotech/ChemLib**

*182078*

*mg*

**From:** Chernyshev, Olga  
**Sent:** Monday, March 13, 2006 4:47 PM  
**To:** STIC-Biotech/ChemLib  
**Subject:** 10/721,297, sequence search request

**Please search SEQ ID NO: 1 and SEQ ID NO: 10 in regular databases only.  
Thank you very much!**

*Olga N. Chernyshev, Ph.D.  
AU 1649  
REM 3C89  
2-0870  
mail 4C70*

*RECEIVED  
MAR 14 2006  
STIC*

\*\*\*\*\*  
Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search  
NA# \_\_\_\_\_ AA#: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.<sup>2</sup>

### OM protein - protein search, using SW model

Run on:

March 15, 2006, 20:08:12 ; search time 146.5 Seconds

(without alignments)

33.71 Million cell updates/sec

Title: US-10-721-297-1

Perfect score: 34

Sequence: 1 EYKMDAE 7

Scoring table: BLOSUM62

Gapopen 10.0 , Gapext 0.5

Searched: 216643 seqs, 70528306 residues

Total number of hits satisfying chosen parameters: 216643

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 05\_80;\*  
1: uniprot\_sprot;\*  
2: uniprot\_trembl;\*

- Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	34	100.0	57 1 A4_URSMA	029149 u alzheimer
2	34	100.0	58 1 A4_CANFA	Q28280 c alzheimer
3	34	100.0	58 1 A4_RADIT	Q28748 o alzheimer
4	34	100.0	58 1 A4_SHEP	Q28757 o alzheimer
5	34	100.0	59 1 A4_BOVIN	Q28053 b alzheimer
6	34	100.0	79 2 Q35463 CRICR	Q35463 cricetulus
7	34	100.0	113 2 Q8JH58 CHRSR	Q8JH58 chelydra se
8	34	100.0	218 2 Q8BPU5_MOUSE	Q8BPU5 mus musculus
9	34	100.0	384 2 Q8BPCT7 MOUSE	Q8BPCT7 mus musculus
10	34	100.0	534 2 Q93296 CHICK	Q93296 gallus gallus
11	34	100.0	569 2 Q9PVLI1_CHICK	Q9PVLI1 gallus gallus
12	34	100.0	695 2 Q5R477_PONY	Q5R477 pongo pygmaea
13	34	100.0	695 2 Q6RH29_CANFIA	Q6RH29 canis familiaris
14	34	100.0	695 2 Q6GJK3_CANFIA	Q6GJK3 canis familiaris
15	34	100.0	695 2 Q6GR78_MOUSE	Q6GR78 mus musculus
16	34	100.0	695 2 Q9DG18_CHICK	Q9DG18 gallus gallus
17	34	100.0	714 2 Q56JK4_CANFIA	Q56JK4 canis familiaris
18	34	100.0	733 2 Q6P6Q5 RAT	Q6P6Q5 rattus norvegicus
19	34	100.0	749 2 Q56JK2_STECO	Q56JK2 stenella co
20	34	100.0	751 1 A4_SA1SC	Q95341 s amyloid beta
21	34	100.0	751 2 Q6GSCO_HUMAN	Q6GSCO homo sapiens
22	34	100.0	751 2 Q6RH28_CANFIA	Q6RH28 canis familiaris
23	34	100.0	751 2 Q56JK5_CANFIA	Q56JK5 canis familiaris
24	34	100.0	751 2 Q4R4R8_MACFIA	Q4R4R8 macaca fasciata
25	34	100.0	751 2 Q9DG17_CHICK	Q9DG17 gallus gallus
26	34	100.0	770 1 A4_CAVFO	Q60595 c amyloid beta
27	34	100.0	770 1 A4_HUMAN	Q60597 h amyloid beta
28	34	100.0	770 1 A4_MACFIA	P55601 m amyloid beta
29	34	100.0	770 1 A4_MOUSE	P12023 m amyloid beta
30	34	100.0	770 1 A4_PANTR	Q55880 p amyloid beta
31	34	100.0	770 1 A4_PIG	P79307 s amyloid beta

### ALIGNMENTS

32	34	100.0	770 1 A4_RAT	P08592 r amyloid beta
33	34	100.0	770 2 Q6RH30_CANFA	Q6RH30 canis familiaris
34	34	100.0	770 2 Q56JK6_CANFA	Q56JK6 canis familiaris
35	34	100.0	770 2 Q53ZT3_MOUSE	Q53ZT3 mus musculus
36	34	100.0	770 2 Q547B7_RAT	Q547B7 ratmus norvegicus
37	34	91.2	119 2 Q8ZZP0_PYRAE	Q8ZZP0 pyracanthus
38	34	91.2	336 2 Q6PC00_BRARE	Q6PC00 brachydontis
39	34	91.2	354 2 Q4SK78_TEING	Q4SK78 teiroides
40	34	91.2	693 2 Q98SG0_XENILA	Q98SG0 xenopus laevis
41	34	91.2	695 2 Q98SF9_XENILA	Q98SF9 xenopus laevis
42	34	91.2	695 2 Q7ZXQ0_XENILA	Q7ZXQ0 xenopus laevis
43	34	91.2	747 2 Q91963_9PIPI	Q91963 xenopus laevis
44	34	91.2	749 2 Q6NRRI_XENITA	Q6NRRI xenopus laevis
45	34	91.2	750 2 Q6DJB6_XENTR	Q6DJB6 xenopus laevis





page 2

## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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; PRIOR FILING DATE: 1999-09-23 ; CURRENT APPLICATION NUMBER: US/09/416,901B
; PRIOR APPLICATION NUMBER: US 09/404,133 ; CURRENT FILING DATE: 1999-10-13
; PRIOR FILING DATE: 1999-09-23 ; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR APPLICATION NUMBER: PCT/US99/20881 ; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23 ; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1998-09-24 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
; NUMBER OF SEQ ID NOS: 73 ; PRIOR FILING DATE: 1999-09-23
; SOFTWARE: PatentIn version 3.1 ; PRIOR APPLICATION NUMBER: US 60/101,594
; SEQ ID NO 67 ; PRIOR FILING DATE: 1998-09-24
; LENGTH: 8 ; NUMBER OF SEQ ID NOS: 72
; TYPE: PRT ; SOFTWARE: PatentIn version 3.1
; ORGANISM: Artificial sequence ; SEQ ID NO 67
; FEATURE: ; LENGTH: 8
; OTHER INFORMATION: Peptide ; TYPE: PRT
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; Best Local Similarity 100.0%; Pred. No. 4.6e+05;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVKMDAE 7
Db 1 EVKMDAE 7

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; Sequence 67, Application US/09551853D
Patent No. 6509667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE: Peptide
; OTHER INFORMATION: Peptide
; US-09-551-853D-67

RESULT 4
US-09-416-901B-67
; Sequence 67, Application US/09416901B
; Patent No. 6509671
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; CURRENT APPLICATION NUMBER: PCT/US99/20881
; CURRENT FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE: Peptide
; OTHER INFORMATION: Peptide
; US-09-551-853D-67

RESULT 5
US-09-548-316D-67
; Sequence 67, Application US/09548376D
; Patent No. 6706485
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; CURRENT APPLICATION NUMBER: US/09/548,376D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
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; US-09-551-853D-67

RESULT 6
US-09-794-927A-67
; Sequence 67, Application US/09794927A
; Patent No. 6720704
; GENERAL INFORMATION:

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Perfect score: 34  
Sequence: 1 EVRNDAE 7  
Scoring table: BLOSUM62  
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Searched: 572060 seqs., 8275769 residues  
total number of hits satisfying chosen parameters: 572060  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

**Issued Patents AA:\***

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2: /cgn2\_6/ptodata/1/iaa/R\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/iaa/R\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/iaa/PCTMS\_COMB.pep: \*  
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6: /cgn2\_6/ptodata/1/iaa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES					
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2	34	100.0	8	US-09-548-367D-67	Sequence 67, I
3	34	100.0	8	US-09-551-853D-67	Sequence 67, I
4	34	100.0	8	US-09-416-901B-67	Sequence 67, I
5	34	100.0	8	US-09-548-376D-67	Sequence 67, I
6	34	100.0	8	US-09-794-927A-67	Sequence 67, I
7	34	100.0	8	US-09-448-373D-67	Sequence 67, I
8	34	100.0	8	US-09-795-847B-67	Sequence 67, I
9	34	100.0	8	US-09-869-414-67	Sequence 67, I
10	34	100.0	8	US-09-448-336F-67	Sequence 67, I
11	34	100.0	8	US-09-548-368D-67	Sequence 67, I
12	34	100.0	8	US-09-794-925A-67	Sequence 67, I
13	34	100.0	8	US-09-689-314C-70	Sequence 70, I
14	34	100.0	8	US-09-794-734-67	Sequence 67, I
15	34	100.0	9	US-08-802-981-221	Sequence 67, I
16	34	100.0	9	US-09-294-987-6	Sequence 67, I
17	34	100.0	9	US-09-724-956A-82	Sequence 67, I
18	34	100.0	9	US-09-471-668A-82	Sequence 67, I
19	34	100.0	10	US-08-053-321C-64	Sequence 64, F
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## SUMMARIES

572060

ALIGNMENTS

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; Sequence 67, Application US/09548372D
; Patent No. 6420334

; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide
; US-09-548-372D-67

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Best local Similarity 100.0%; Pred. No. 4 6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 EVKMDAE 7
Db      1 EVKMDAE 7

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; Sequence 67, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR APPLICATION NUMBER: US 60/155,493

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PRIOR FILING DATE: 1999-10-13  
; PRIOR APPLICATION NUMBER: 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,594  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 67  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide

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; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OQ 1 EVKMDAE 7  
Db 1 EVKMDAE 7

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Sequence 67, Application US/09795847  
; Patent No. US20010018208A1  
; GENERAL INFORMATION:  
; APPLICANT: Gurney, Mark E.  
; APPLICANT: Bienkowski, Michael J.  
; APPLICANT: Heinrikson, Robert L.  
; APPLICANT: Parodi, Luis A.  
; APPLICANT: Yan, Riqiang  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND FILE REFERENCE: 28341/6280BC  
; CURRENT APPLICATION NUMBER: US/09/794,743  
; CURRENT FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: 09/416,901  
; PRIOR FILING DATE: 1999-10-13  
; PRIOR APPLICATION NUMBER: 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
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; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,594  
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; PRIOR FILING DATE: 1998-09-24  
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; ORGANISM: Artificial Sequence  
; FEATURE:  
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; Patent No. US2002003715A1  
; GENERAL INFORMATION:  
; APPLICANT: Gurney, Mark E.  
; APPLICANT: Bienkowski, Michael J.  
; APPLICANT: Heinrikson, Robert L.  
; APPLICANT: Parodi, Luis A.  
; APPLICANT: Yan, Riqiang  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND FILE REFERENCE: 28341/62800J  
; CURRENT APPLICATION NUMBER: US/09/794,748  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: 09/416,901  
; PRIOR FILING DATE: 1999-10-13  
; PRIOR APPLICATION NUMBER: 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0

Query Match 100.0%; Score 34; DB 3; Length 8;  
; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;  
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OQ 1 EVKMDAE 7  
Db 1 EVKMDAE 7

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### OM protein - protein search, using sw model

Run on: March 15, 2006, 20:18:47 ; Search time 120 Seconds

(without alignments) 24.373 Million cell updates/sec

Title: US-10-721-297-1

Perfect score: 34

Sequence: 1 EVKMDAE 7

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Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA\_Main:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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Query Match

Length

DB ID

Description

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RESULT 1  
US-10-625-854-195  
; Sequence 195, Application US/10625854  
; Publication No. US20050175626A1  
; GENERAL INFORMATION:  
; APPLICANT: delacourte, Andr

; TITLE OF INVENTION: prevention, treatment and diagnosis of diseases associated with beta-amyloid formation and/or aggregation

; FILE REFERENCE: 11362.0039.4NFSU01 (INNS0394--)

; CURRENT APPLICATION NUMBER: US/10/625,854

; PRIORITY APPLICATION NUMBER: European Patent Application No. 02447147.6

; PRIORITY FILING DATE: 2002-07-24

; PRIORITY FILING DATE: 2002-08-06

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 195  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: homo sapiens

US-10-625-854-195

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Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAE 7

Dy 1 EVKMDAE 7

Sequence 67, Appl

Sequence 52, Appl

Sequence 67, Appl

RESULT 2  
US-09-794-927-67

; Sequence 67, Application US/09794927

; Patient No. US2001016324A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Blenkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Paoli, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND

; USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341L6289PG

; CURRENT APPLICATION NUMBER: US/09/794,927

; CURRENT FILING DATE: 2001-02-27

; PRIORITY APPLICATION NUMBER: 09/416,901

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30 34 100.0 10 3 US-09-794-743-64 Sequence 64, Appl  
31 34 100.0 10 3 US-09-794-748-64 Sequence 64, Appl  
32 34 100.0 10 3 US-09-795-264-64 Sequence 64, Appl  
33 34 100.0 10 3 US-09-794-925-64 Sequence 64, Appl  
34 34 100.0 10 3 US-09-845-255-64 Sequence 4, Appl  
35 34 100.0 10 3 US-09-795-903A-20 Sequence 4, Appl  
36 34 100.0 10 3 US-09-908-943A-20 Sequence 20, Appl  
37 34 100.0 10 3 US-09-859-415-64 Sequence 64, Appl  
38 34 100.0 10 3 US-09-548-366-64 Sequence 64, Appl  
39 34 100.0 10 3 US-10-042-205-53 Sequence 7, Appl  
40 34 100.0 10 4 US-10-652-927-64 Sequence 53, Appl  
41 34 100.0 10 4 US-10-652-830-64 Sequence 64, Appl  
42 34 100.0 10 4 US-10-281-092-12 Sequence 64, Appl  
43 34 100.0 10 4 US-10-653-045-64 Sequence 12, Appl  
44 34 100.0 10 4 US-10-653-045-64 Sequence 64, Appl  
45 34 100.0 10 4 US-10-653-045-64 Sequence 64, Appl

(I) has neuroprotective and nootropic activities, and can be used in gene therapy. (I) can be used for producing preparations of homogeneously processed BACE that may be used for e.g. studying or treating diseases such as Alzheimer's disease or Down's syndrome. The human BACE1 gene is located on chromosome 11, more specifically to 11q22.2-23.3. The present sequence represents a human BACE1 autoproteolysis site amino acid sequence, which is used in the exemplification of the present invention.

SQ Sequence 7 AA:

Query Match 100.0%; Score 34; DB 8; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVNLDAE 7

Db 1 EVNLDAE 7

RESULT 2  
AER23394  
ID AER23394 standard; peptide; 7 AA.  
XX AC  
XX DT 28-JUL-2005 (first entry)  
XX DE Human APP beta-secretase cleavage site mutant peptide #2.  
XX KW Screening; beta-amyloid; amyloid precursor protein; neuroprotective; nootropic; degeneration; neurological disease; beta-secretase; mutein.  
XX OS Homo sapiens.  
XX PN US200512696-A1.  
XX PD 26-MAY-2005.  
XX PP 25-NOV-2003; 2003US-00721297.  
PR 25-NOV-2003; 2003US-00721297.  
XX PA (UNIV TEXAS SOUTHWESTERN MEDICAL CENT DAL.  
XX PI Sudhof TC, Li Q;  
XX DR WPI; 2005-493362/41.  
XX PT Identifying agents modulating cleavage of amyloid beta-precursor protein by beta-secretase, by contacting chimeric molecule comprising cleavage site with beta-secretase in presence of modulating agent, measuring PT nuclear localization.  
XX PS Claim 3; page 10; 20pp; English.

The present invention relates to a method of screening and identifying agents that modulate cleavage of amyloid beta-precursor protein (APP) or APP-like proteins such as APP1 and APP2 by a beta-secretase. The method involves contacting a chimeric molecule comprising a transmembrane region (TMR) with a gamma- or beta-secretase cleavage site and an APP C-terminal cytoplasmic tail modified with beta-secretase in presence and absence of a modulating agent and identifying cleavage by measuring nuclear localization of C-terminal cytoplasmic tail. The invention is useful in the treatment of Alzheimer's disease. The present sequence is the human APP beta-secretase cleavage site peptide containing swedish mutation.

XX SQ Sequence 7 AA:

Query Match 100.0%; Score 34; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVNLDAE 7  
Db 1 EVNLDAE 7

RQ RESULT 3  
ID AERB09785 standard; peptide; 7 AA.  
XX AC AERB09785;  
XX DT 08-SEP-2005 (first entry)  
XX DE Autoproteolysis sequence for engineered BACE1, SEQ ID 21.  
XX KW Protein engineering; Beta secretase; amyloid precursor protein; Alzheimer's disease; Down syndrome; neuroprotective; nootropic; autoproteolytic site.  
XX OS Homo sapiens.  
XX PN WO200500384-A2.  
XX PD 07-JUL-2005.  
XX PR 07-JUL-2004; 2004WO-US021816.  
XX PR 02-DEC-2003; 2003US-00726967.  
XX PA (SUNE-) SUNESTS PHARM INC.  
XX PI Ballinger M, Randal ML;  
XX DR WPI; 2005-497667/50.  
XX PT New polypeptide having beta site amyloid precursor protein APP-cleaving enzyme (BACE) activity, having a prodomain, and autoproteolysis site and protease domain, for producing preparations of homogeneously processed BACE.  
XX PS Claim 12; SEQ ID NO 21; 71pp; English.  
CC The invention relates to a polypeptide (1) comprising in order from N-terminus to C-terminus, a prodomain (comprising at least six contiguous amino acids of AEBB09767), an autoproteolysis site and a protease domain (comprising at least one amino acid sequence chosen from a sequence at least 90% identical to residues 74-207, 241-361 or 309-446 of AERB09765), where the polypeptide is capable of being cleaved at the autoproteolysis site to thus release a free protease domain that has beta site amyloid precursor protein (APP)-cleaving enzyme (BACE, beta secretase) activity. Also included are a nucleic acid sequence encoding the polypeptide, a vector for expressing the polypeptide and a host cell expressing the polypeptide. The polypeptide is useful for producing preparations of homogeneously processed BACE, and for cleaving amyloid precursor protein at its beta-secretase site, to liberate Abeta peptide, where the cerebral deposition of Abeta peptide causes Alzheimer's disease and Down's syndrome. The polypeptide comprises a prodomain, an engineered cleavage site and a protease domain. The polypeptide is properly folded and is cleaved at the engineered cleavage site in vitro, to produce homogeneous preparations of purified protease having BACE activity. The present sequence is an autoproteolytic cleavage site which may be engineered into the polypeptide of the invention.

CC SQ Sequence 7 AA:

Query Match 100.0%; Score 34; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVNLDAE 7  
Db 1 EVNLDAE 7

GenCore version 5.1.7  
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## OM protein - protein search, using sw model

Run on: March 15, 2006, 20:07:46 ; Search time 135 Seconds  
(without alignments)

22.783 Million cell updates/sec

Title: US-10-721-297-10

Perfect score: 34 EVNLDAE 7

Sequence: BLOSUM62

Gapov 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378761 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_GenSeq\_21:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2008s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003s:\*
- 7: geneseqp2003s:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	34	100.0	7 8 ADP83933	Adp83933 Human BAC
2	34	100.0	7 9 AEA23394	Aea23394 Human APP
3	34	100.0	7 9 AEP07985	Aep07985 Autoprotease
4	34	100.0	8 3 AAY94771	Aay94771 Beta-secr
5	34	100.0	8 4 AAEI0661	Aaei0661 Human asp
6	34	100.0	8 4 AAB05613	Aab05613 Human Asp
7	34	100.0	8 5 ABB78622	Abb78622 Human bet
8	34	100.0	8 6 ABR5159	Ab5159 Beta-secr
9	34	100.0	8 9 AEA23385	Aea23385 Human APP
10	34	100.0	9 2 AAWB2081	AAWB2081 Fluorogen
11	34	100.0	9 3 AAB07874	Aab07874 A peptide
12	34	100.0	9 3 AAGT0894	Aagt0894 Substrate
13	34	100.0	9 4 AAGT3297	Aagt3297 Protease
14	34	100.0	9 5 ABB06519	Abb06519 Beta-secr
15	34	100.0	9 5 ABB09003	Abb09003 Peptide #
16	34	100.0	9 5 ABU60429	Abu60429 Protease
17	34	100.0	9 5 ABU60441	Abu60441 Protease
18	34	100.0	9 5 AAE16663	Aae16663 Oligopept
19	34	100.0	9 5 AAT74837	Aat74837 Synthetic
20	34	100.0	9 5 ABB07598	Abb07598 Synthetic
21	34	100.0	9 5 AAM0897	Aam0897 Oligopept
22	34	100.0	9 6 ABP97975	Abp97975 Synthetic
23	34	100.0	9 6 ABP57515	Abp57515 Different
24	34	100.0	9 6 ABP57084	Abp57084 Synthetic

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_GenSeq\_21:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2008s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003s:\*
- 7: geneseqp2003s:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	34	100.0	7 8 ADP83933	ADP83933 standard; peptide; 7 AA.
2	34	100.0	7 9 AEA23394	ID ADP83933; XX
3	34	100.0	7 9 AEP07985	XX AC ADP83933;
4	34	100.0	8 3 AAY94771	XX DT 23-SBP-2004 (first entry)
5	34	100.0	8 4 AAEI0661	XX DB Human BACE1 autoproteolysis site SEQ ID NO:59.
6	34	100.0	8 4 AAB05613	XX KW human; beta-site amyloid precursor protein cleaving enzyme 1; beta-site amyloid precursor protein cleavage site; protease domain; neuroprotective; gene therapy; Alzheimer's disease; Down's syndrome.
7	34	100.0	8 5 ABB78622	XX KW engineered cleavage site; protease domain; neuroprotective; nootropic; gene therapy; Alzheimer's disease; Down's syndrome.
8	34	100.0	8 6 ABR5159	XX OS Homo sapiens.
9	34	100.0	8 9 AEA23385	XX PN WO2004056962-A2.
10	34	100.0	9 2 AAWB2081	XX PD 08-JUL-2004.
11	34	100.0	9 3 AAB07874	XX PR 02-DEC-2003; 2003WO-US038314.
12	34	100.0	9 3 AAGT0894	XX PR 04-DEC-2002; 2002US-0430984P.
13	34	100.0	9 4 AAGT3297	XX PT (SUNB-) SUNESIS PHARM INC.
14	34	100.0	9 5 ABB06519	XX PT Ballinger M;
15	34	100.0	9 5 ABB09003	XX DR WPI; 2004-507703/48.
16	34	100.0	9 5 ABU60429	XX PT New polypeptides for producing homogeneously processed preparations of beta-site amyloid precursor protein cleavage site and a protease domain.
17	34	100.0	9 5 ABU60441	XX PT predomain, an engineered cleavage site and a protease domain.
18	34	100.0	9 5 AAE16663	XX PT claim 10; SEQ ID NO 59; 40pp; English.
19	34	100.0	9 5 AAT74837	XX CC The present invention describes a polypeptide (1) comprising in order from the N-terminus to the C-terminus: (a) a predomain comprising at least 6 contiguous amino acids of the 16 amino acid sequence of SEQ ID NO:3 (ADP8387), comprising residues 22-37 of SEQ ID NO:1 (ADP83876) which is the longest isoform of human beta-site amyloid precursor protein (APP) cleaving enzyme 1 (BACE1), isoform A; (b) an engineered cleavage site; and (c) a protease domain. (1) is capable of being cleaved at the engineered cleavage site, and so releases a free protease domain that has BACE1 activity. Also described: (1) a nucleic acid sequence encoding (1);
20	34	100.0	9 5 ABB07598	CC (2) a vector for expression of (1); and (3) a host cell expressing (1).
21	34	100.0	9 5 AAM0897	CC
22	34	100.0	9 6 ABP97975	CC
23	34	100.0	9 6 ABP57515	CC
24	34	100.0	9 6 ABP57084	CC

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_GenSeq\_21:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2008s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003s:\*
- 7: geneseqp2003s:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*

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## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	34	100.0	7 8 ADP83933	ADP83933 standard; peptide; 7 AA.
2	34	100.0	7 9 AEA23394	AC ADP83933;
3	34	100.0	7 9 AEP07985	DT 23-SBP-2004 (first entry)
4	34	100.0	8 3 AAY94771	XX DB Human BACE1 autoproteolysis site SEQ ID NO:59.
5	34	100.0	8 4 AAEI0661	XX KW human; beta-site amyloid precursor protein cleaving enzyme 1; beta-site amyloid precursor protein cleavage site; protease domain; neuroprotective; gene therapy; Alzheimer's disease; Down's syndrome.
6	34	100.0	8 5 ABB78622	XX KW engineered cleavage site; protease domain; neuroprotective; nootropic; gene therapy; Alzheimer's disease; Down's syndrome.
7	34	100.0	8 6 ABR5159	XX OS Homo sapiens.
8	34	100.0	8 9 AEA23385	XX PN WO2004056962-A2.
9	34	100.0	9 2 AAWB2081	XX PD 08-JUL-2004.
10	34	100.0	9 3 AAB07874	XX PR 02-DEC-2003; 2003WO-US038314.
11	34	100.0	9 3 AAGT0894	XX PR 04-DEC-2002; 2002US-0430984P.
12	34	100.0	9 4 AAGT3297	XX PT (SUNB-) SUNESIS PHARM INC.
13	34	100.0	9 5 ABB06519	XX PT Ballinger M;
14	34	100.0	9 5 ABB09003	XX DR WPI; 2004-507703/48.
15	34	100.0	9 5 ABU60429	XX PT New polypeptides for producing homogeneously processed preparations of beta-site amyloid precursor protein cleavage site and a protease domain.
16	34	100.0	9 5 ABU60441	XX PT predomain, an engineered cleavage site and a protease domain.
17	34	100.0	9 5 AAE16663	XX PT claim 10; SEQ ID NO 59; 40pp; English.
18	34	100.0	9 5 AAT74837	CC The present invention describes a polypeptide (1) comprising in order from the N-terminus to the C-terminus: (a) a predomain comprising at least 6 contiguous amino acids of the 16 amino acid sequence of SEQ ID NO:3 (ADP83877), comprising residues 22-37 of SEQ ID NO:1 (ADP83876) which is the longest isoform of human beta-site amyloid precursor protein (APP) cleaving enzyme 1 (BACE1), isoform A; (b) an engineered cleavage site; and (c) a protease domain. (1) is capable of being cleaved at the engineered cleavage site, and so releases a free protease domain that has BACE1 activity. Also described: (1) a nucleic acid sequence encoding (1);
19	34	100.0	9 5 ABB07598	CC (2) a vector for expression of (1); and (3) a host cell expressing (1).
20	34	100.0	9 5 AAM0897	CC
21	34	100.0	9 6 ABP97975	CC
22	34	100.0	9 6 ABP57515	CC
23	34	100.0	9 6 ABP57084	CC

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_GenSeq\_21:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2008s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003s:\*
- 7: geneseqp2003s:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*

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## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	34	100.0	7 8 ADP83933	ADP83933 standard; peptide; 7 AA.
2	34	100.0	7 9 AEA23394	AC ADP83933;
3	34	100.0	7 9 AEP07985	DT 23-SBP-2004 (first entry)
4	34	100.0	8 3 AAY94771	XX DB Human BACE1 autoproteolysis site SEQ ID NO:59.
5	34	100.0	8 4 AAEI0661	XX KW human; beta-site amyloid precursor protein cleaving enzyme 1; beta-site amyloid precursor protein cleavage site; protease domain; neuroprotective; gene therapy; Alzheimer's disease; Down's syndrome.
6	34	100.0	8 5 ABB78622	XX KW engineered cleavage site; protease domain; neuroprotective; nootropic; gene therapy; Alzheimer's disease; Down's syndrome.
7	34	100.0	8 6 ABR5159	XX OS Homo sapiens.
8	34	100.0	8 9 AEA23385	XX PN WO2004056962-A2.
9	34	100.0	9 2 AAWB2081	XX PD 08-JUL-2004.
10	34	100.0	9 3 AAB07874	XX PR 02-DEC-2003; 2003WO-US038314.
11	34	100.0	9 3 AAGT0894	XX PR 04-DEC-2002; 2002US-0430984P.
12	34	100.0	9 4 AAGT3297	XX PT (SUNB-) SUNESIS PHARM INC.
13	34	100.0	9 5 ABB06519	XX PT Ballinger M;
14	34	100.0	9 5 ABB09003	XX DR WPI; 2004-507703/48.
15	34	100.0	9 5 ABU60429	XX PT New polypeptides for producing homogeneously processed preparations of beta-site amyloid precursor protein cleavage site and a protease domain.
16	34	100.0	9 5 ABU60441	XX PT predomain, an engineered cleavage site and a protease domain.
17	34	100.0	9 5 AAE16663	XX PT claim 10; SEQ ID NO 59; 40pp; English.
18	34	100.0	9 5 AAT74837	CC The present invention describes a polypeptide (1) comprising in order from the N-terminus to the C-terminus: (a) a predomain comprising at least 6 contiguous amino acids of the 16 amino acid sequence of SEQ ID NO:3 (ADP83877), comprising residues 22-37 of SEQ ID NO:1 (ADP83876) which is the longest isoform of human beta-site amyloid precursor protein (APP) cleaving enzyme 1 (BACE1), isoform A; (b) an engineered cleavage site; and (c) a protease domain. (1) is capable of being cleaved at the engineered cleavage site, and so releases a free protease domain that has BACE1 activity. Also described: (1) a nucleic acid sequence encoding (1);
19	34	100.0	9 5 ABB07598	CC (2) a vector for expression of (1); and (3) a host cell expressing (1).
20	34	100.0	9 5 AAM0897	CC
21	34	100.0	9 6 ABP97975	CC
22	34	100.0	9 6 ABP57515	CC
23	34	100.0	9 6 ABP57084	CC

## RESULT 3

H86169 hypothetical protein [imported] - *Arabidopsis thaliana*;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Accession: H86169 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C;Date: 02-Mar-2001

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

N;Nature 399, 322-329, 1999

A;Reference number: A72200; MUID:9287316; PMID:10360771

A;Accession: A72411

A;Status: preliminary

A;Molecule type: DNA

A;Accession: A7278 &lt;ARN&gt;

A;Cross-references: UNIPROT:Q9WY10; UNIPARC:UPI00000C146F; GB:AE001701; GB:AE000512; NID

A;Experimental source: strain MSBB

C;Genetics: TM0163

A;Gene: TM0163

Query Match 91.2%; Score 31; DB 2; Length 672;

Best Local Similarity 85.7%; Pred. No. 61;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAE 7

Db 538 EVNLSE 544

A;Residues: 1-572 &lt;STO&gt;

A;Cross-references: UNIPROT:Q9ZWB1; UNIPARC:UPI00000A06K; GB:AE005172; NID:94204304; PI

C;Genetics:

A;Map position: 1

Query Match 91.2%; Score 31; DB 2; Length 672;

Best Local Similarity 85.7%; Pred. No. 38;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: H86169

A;Status: preliminary

A;Molecule type: DNA

A;Accession: A72411

A;Cross-references: UNIPROT:Q9WY10; UNIPARC:UPI00000C146F; GB:AE001701; GB:AE000512; NID

A;Experimental source: strain MSBB

C;Genetics: TM0163

A;Gene: TM0163

Query Match 89.2%; Score 30; DB 2; Length 278;

Best Local Similarity 85.7%; Pred. No. 38;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVNLDAE 7

Db 241 EVNLDE 247

## RESULT 4

T18555

hypothetical protein B0035.4 - *Caenorhabditis elegans*C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T18655

C;Submitted to the EMBL Data Library, May 1996

A;Reference number: 219002

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-126 &lt;WTI&gt;

A;Cross-references: UNIPROT:Q17435; UNIPARC:UPI000131727; EMBL:273102; PDB:CAA97410.1;

A;Experimental source: clone B0035

A;Genetics:

A;Gene: C1SP:B0035.4

A;Map position: 4

A;Introns: 29/3; 73/3

C;Superfamily: *Arabidopsis thaliana* hypothetical protein F22013.29

## RESULT 5

A72411

hypothetical protein - *Thermotoga maritima* (strain MSB9)C;Species: *Thermotoga maritima*

C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

A;Title: Genome sequence of an obligate intracellular pathogen of humans: *Chlamydia trac*

A;Reference number: A71570; MUID:99000809; PMID:9784136

A;Accession: H71516

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-497 &lt;ARN&gt;

A;Cross-references: UNIPROT:Q9PJJW0; UNIPARC:UPI000057A25; GB:AE002340; GB:AE002160; NID

A;Experimental source: strain Nigg (MOPN)

C;Genetics:

A;Gene: T00716

A;Superfamily: serine/glycine hydroxymethyltransferase

## RESULT 6

C81672

serine hydroxymethyltransferase TC0716 [imported] - *Chlamydia muridarum* (strain Nigg)C;Species: *Chlamydia muridarum*, *Chlamydia trachomatis* MoPn

C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C;Accession: C01672

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of *Chlamydia trachomatis* MoPn and *Chlamydia pneumoniae* AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: C01672

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-497 &lt;TEET&gt;

A;Cross-references: UNIPROT:Q9PJJW0; UNIPARC:UPI000057A25; GB:AE002340; GB:AE002160; NID

A;Experimental source: strain Nigg (MOPN)

C;Genetics:

A;Gene: T00716

A;Superfamily: serine/glycine hydroxymethyltransferase

## RESULT 7

H71516

glycine hydroxymethyltransferase (EC 2.1.2.1) - *Chlamydia trachomatis* (serotype D, strain

N;Alternate names: serine hydroxymethyltransferase

C;Species: *Chlamydia trachomatis*

C;Date: 11-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004

C;Accession: H71516

R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Pan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 262, 754-759, 1998

A;Title: Genome sequence of an obligate intracellular pathogen of humans: *Chlamydia trac*

A;Reference number: A71570; MUID:99000809; PMID:9784136

A;Accession: H71516

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-497 &lt;ARN&gt;

A;Cross-references: UNIPROT:Q84439; UNIPARC:UPI00012B85B; GB:AB001316; GB:AE001273; NID

A;Experimental source: serotype D, strain UW-3/Cx

C;Genetics:

A;Gene: GLYA

C;Superfamily: serine/glycine hydroxymethyltransferase

GenCore version 5.1.7  
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## OM protein - protein search, using sw model

Run on: March 15, 2006, 20:13:01 ; Search time 24 Seconds  
 (without alignments)  
 28.063 Million cell updates/sec

Title: US-10-721-297-10  
 Perfect score: 34  
 Sequence: EVNLDAE 7

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_80;\*  
 1: pir1;\*  
 2: pir2;\*  
 3: pir3;\*  
 4: pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	% Match	Length	DB ID	Description
1	34	100.0	419	2	D42725	nitrile hydratase
2	31	91.2	368	2	A20825	keratin, type I no
3	31	91.2	672	2	H86169	hypothetical prote
4	30	88.2	126	2	T18655	hypothetical prote
5	30	88.2	278	2	A72411	hypothetical prote
6	30	88.2	81672	2	C81672	serine hydroxymethyl
7	30	88.2	497	2	H1516	glycine hydroxymethyl
8	30	88.2	802	2	C90326	hypothetical prote
9	29	85.3	282	2	T26112	hypothetical prote
10	29	85.3	289	2	D68795	transcription regu
11	29	85.3	295	2	F83867	dihydrodipicolinate
12	29	85.3	326	2	A83087	conserved hypothet
13	29	85.3	340	2	T35558	DNA-directed RNA p
14	29	85.3	394	2	F89888	alanine racemase h
15	29	85.3	400	2	E5099	ribosomal protein
16	29	85.3	400	2	D97967	30S ribosomal prot
17	29	85.3	434	2	D88305	protein R03D7.4 (li
18	29	85.3	434	2	A23430	transcription elon
19	29	85.3	442	2	B82633	nitrile hydratase
20	29	85.3	470	2	C75591	threonine synthase
21	29	85.3	408	2	B96658	hypothetical prote
22	29	85.3	550	2	A03494	olopeptide trans
23	29	85.3	619	1	JH0776	hydrogenase (EC 1.
24	29	85.3	712	2	H8776	DNA grasse subunit
25	29	85.3	712	2	H97555	DNA grasse chain b
26	29	85.3	743	2	D64062	GMP diphosphokinase
27	29	85.3	929	2	T25217	hypothetical prote
28	29	85.3	1331	2	H82211	sensory box sensor
29	82.4					molybdenum cofactor

## ALIGNMENTS

Qry	1	EVNLDAE 7	Db	48	EVNLDAE 54
RESULT 1					
D42725					
nitrile hydratase region 3'-hypothetical protein P47K - <i>Pseudomonas chlororaphis</i> (strain					
C;Species: <i>Pseudomonas chlororaphis</i>					
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004					
C;Accession: D42725					
R;Nishiyama, M.; Horinouchi, S.; Kobayashi, M.; Nagasawa, T.; Yamada, H.; Beppu, T.					
J;Bacteriol. 173, 2465-2472, 1991					
A;Title: Cloning and characterization of genes responsible for metabolism of nitrile co-					
A;Reference number: A42725; MID:91193202; PMID:2013568					
A;Status: Preliminary; not compared with conceptual translation					
A;Molecule type: DNA					
A;Residues: 1-419 <NLS>					
A;Cross-references: UNIPROT:P31521; UNIPARC:UPI000013102A; GB:D90216; NID:9216850; PIDN:					
C;Superfamily: conserved hypothetical protein yciC					
Query Match 100%; Score 34; DB 2; Length 419;					
Best Local Similarity 100%; Pred. No. 7.3; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					

DT 13-SEP-2005 (TREMBLrel. 31, last sequence update)

DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)

DE Transcription factor protein.

GN Name=Ci-ARP3;

OS Ciona intestinalis.

OC Eukaryota; Metazoa; Chordata; Urochordata; Asciidae; Enterogona; Phlebobranchia; Cionidae; Ciona.

OX NCBI\_TaxID=7719;

RN [1]

NUCLEOTIDE SEQUENCE ID Q8PYH8 METMA PRELIMINARY; PRT; 84 AA.

Pubmed=15269171; DOI=10.1242/dev.01270; Imai K.S.; Hino K.; Yagi K.; Satoh N.; Satou Y.; "Genome-wide surveys of developmentally relevant genes in Ciona intestinalis"; Development 131:4047-4058(2004).

RN [2]

NUCLEOTIDE SEQUENCE ID Q8PYH8 METMA PRELIMINARY; PRT; 84 AA.

Pubmed=12736827; DOI=10.1007/s00427-003-0330-z; Satoh Y.; Satoh N.; "Genome-wide surveys of developmentally relevant genes in Ciona intestinalis." Dev. Genes Evol. 213:211-212(2003).

RN [3]

NUCLEOTIDE SEQUENCE ID Q8PYH8 METMA PRELIMINARY; PRT; 84 AA.

RA Satoh Y.; "Expressed genes in Ciona intestinalis"; Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.

RL EMBL: AB210313; BAE06318 1; -; mRNA.

SQ SEQUENCE 273 AA; 31974 MW; 4D5C47CC9B77361 CRC64;

Query Match 97.1%; Score 33; DB 2; Length 273; Best Local Similarity 85.7%; Pred. No. 67; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAE 7

Db 217 BINLDAE 223

RESULT 3

Q6NSG6\_RIOPA ID Q6NSG6\_RIOPA PRELIMINARY; PRT; 402 AA.

AC 06NSG6;

DT 05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DE Hypothetical protein

GN OrderdLocusName=RRIAL462;

OS Rhodopseudomonas palustris.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Rhodopseudomonas.

OX NCBI\_TaxID=1076;

RN [1]

NUCLEOTIDE SEQUENCE ID STRAIN=CGA009 / ATCC BAA-199; PRT; 402 AA.

Pubmed=14704707; DOI=10.1038/bt923; Larimer F.W., Chain P., Hauser L., Lamedrin J.E., Malfatti S., Do L., Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabata F.R., Gibson J.L., Hanson T.E., Bobat C., Torres Y Torres J.L., Peres C., Harrison R.H., Gibson J.J., Harwood C.S.; "Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris.;" Nat. Biotechnol. 22:655-61(2004).

DR InterPro: IPR003495; CobW\_Pfam; PF0492; cobW\_1.

DR Pfam; PF0492; cobW\_1.

DR Pfam; PF0683; CobW\_C; 1.

DR Complete Proteome; Hypothetical protein.

SQ SEQUENCE 402 AA; 45220 MW; 6D5A48B1887791B CRC64;

Query Match 94.1%; Score 32; DB 2; Length 402; Best Local Similarity 85.7%; Pred. No. 1.7e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVNLDAE 7

Db 78 BINLDAE 84

RESULT 5

Q8TIN2\_METAC ID Q8TIN2\_METAC PRELIMINARY; PRT; 84 AA.

AC Q8TIN2;

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Predicted protein.

GN OrderdLocusName=MA402B;

OS Methanocarcina acetiivorans.

OC Archaea; Buryarchaeota; Methanomicrobia; Methanocarcinales; Methanococcaceae; Methanocarcina.

OX NCBI\_TaxID=2214;

RN [1]

NUCLEOTIDE SEQUENCE ID STRAIN=C2A / ATCC 35395 / DSM 2834; PRT; 84 AA.

Pubmed=121929760; DOI=10.1101/gr.222902; Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., FitzHugh W., Calvo S., Engel R., Sunirno S., Atreno D., Brown A., Allen N., Naylor J., Strange-Thomann N., Dearellano K., Johnson R., Linton L., McElvan P., McFernan K., Talman J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cain I., Graham D.E., Graham D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuetter H.C., Krzycki J.A., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umeyam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Metcalf W.W., Birren B.; "Complete proteome of the archaeon Methanococcoides burtonii str. N2A." J. Bacteriol. 187:6293-6302(2005).

GenCore version 5.1.7  
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## OM protein - protein search, using sw model

Run on: March 15, 2005, 20:08:12 ; Search time 146.5 Seconds  
(without alignments)  
33.711 Million cell updates/sec

Title: US-10-721-297-10  
Perfect score: 34  
Sequence: 1 EVNLDAE 7

Scoring table: BLOSUM62  
Gapop 10 0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt;05;80;\*  
1: uniprot\_sprot;\*  
2: uniprot\_trembl;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	419	1 P47K_PSECL	P31521; pseudomonas
2	33	97.1	273	2 Q4H3V9_CLOIN	Q4h3v9 cton intes
3	32	94.1	402	2 QEN956_RHOPSA	Q6n9s6 rhodopsedo
4	31	91.2	84	2 Q8PYH8_METMCA	Q8pyh8 methanobarc
5	31	91.2	84	2 QBTIM2_METMCA	Q8tim2 methanobarc
6	31	91.2	118	2 Q4RZ22_TBING	Q4rz22 tbing
7	31	91.2	221	2 Q82W77_NITBU	Q82w77 nitrosoomca
8	31	91.2	225	2 Q8TP55_METACB	Q8tp55 methanobarc
9	31	91.2	281	2 Q8AMO_BACTIN	Q8a4m0 bacterooides
10	31	91.2	368	1 KIC18_XENLA	P08802 xenopus lae
11	31	91.2	402	2 QEBFB_ACTAD	Q6fbu8 actinobact
12	31	91.2	408	2 Q5NG56_FRATT	Q5ng56 francisella
13	31	91.2	428	2 QDINH6_XENLAA	Q6in6 xenopus lae
14	31	91.2	436	2 QAVI2_XENLIA	Q8av12 xenopus lae
15	31	91.2	672	2 Q8WB1I_ARATH	Q9zb1i arabidopsis
16	31	91.2	1154	2 QEMEZO_PARUN	Q6mezo parachlamydy
17	31	91.2	1186	2 Q522M9_WAGGR	Q522m9 magnaporth
18	30	88.2	54	2 QRP193_STRPB	Q8p193 streptococc
19	30	88.2	126	1 P0D4_CALER	Q1745 caenorhabdi
20	30	88.2	126	2 Q61S09_CAEER	Q61s09 caenorhabdi
21	30	88.2	142	2 Q802K3_CAEER	Q602k3 caenorhabdi
22	30	88.2	222	2 Q8CBM3_EMENT	Q5bcm3 aspergillus
23	30	88.2	278	2 Q8CBM4_9THEM	Q5cbm4 thermotoga
24	30	88.2	278	2 Q8CBK6_9THEM	Q5cbk6 thermotoga
25	30	88.2	278	2 Q8CBT8_9THEM	Q5cbt8 thermotoga
26	30	88.2	278	2 Q8WY10_THEME	Q9wy10 thermotoga
27	30	88.2	294	1 P0851_YARLI	Q6ctu8 Yarrowia li
28	30	88.2	330	1 P8052_DDEBA	Q6bty2 dearyonyc
29	30	88.2	372	2 Q5V641_HALMA	Q5v641 haloarcula
30	88.2	497	1 GLYA_CHLMU	Q9pjwo chlamydia m	
31	88.2	497	1 GLYA_CHLMU	Q84439 chlamydia t	

## ALIGNMENTS

RESULT 1  
P47K\_PSECL  
ID: P47K\_PSECL STANDARD; PRT; 419 AA.  
AC: P31521;  
DT: 01-JUL-1993 (Rel. 26, Created)  
DT: 01-JUL-1993 (Rel. 26, Last sequence update)  
DT: 13-SEP-2005 (Rel. 48, Last annotation update)  
DB: 47 kDa protein (P47K)  
OS: Pseudomonas chlororaphis (Pseudomonas aureofaciens).  
OC: Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC: Pseudomonadaceae; Pseudomonas.  
OX: NCBI\_TaxID=333;  
RN: [1]  
RP: NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
STRAIN=B23;  
RC: MEDLINE=91193202; PubMed=2013568;  
RA: Nishiyama M., Horinouchi S., Kobayashi M., Nagabawa T., Yamada H.,  
RA: Beppu T.;  
RT: "Cloning and characterization of genes responsible for metabolism of nitrile compounds from Pseudomonas chlororaphis B23.";  
RL: J. Bacteriol. 173:465-472(1991).  
CC: "The presence of P47K is critical for the expression of the nitrile hydratase genes. May stabilize or activate the nitrile hydratase proteins."  
CC: -----  
CC: This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
CC: -----  
DR: EMBL; D90216; BAA14247.1; -; Genomic\_DNA.  
DR: PIR; D42275; D42275.  
DR: HSSP; P24203; INIJJ.  
DR: InterPro; IPR011629; CobW\_C.  
DR: InterPro; IPR003495; P47K\_Cob\_Synth.  
DR: Pfam; PF02492; cobW\_1.  
DR: Pfam; PF07683; CobW\_C\_1.  
SQ: SEQUENCE 419 AA; MW; FF5113800E27FF0C CRC64;

Query	Match	Best Local Similarity	Score	DB	Length
QY	1 EVNLDAE 7	100.0%	34	DB 1;	419;
QY	1 EVNLDAE 7	100.0%	34	DB 1;	419;
Db	48 EVNLDAE 54	100.0%	34	DB 1;	419;

RESULT 2  
CLOIN  
Q4H3V9\_CLOIN PRELIMINARY; PRT; 273 AA.  
AC: Q4H3V9\_CLOIN  
DT: 13-SEP-2005 (TiEMBLrel. 31, Created)





PRIOR APPLICATION NUMBER: 60/292,591  
 PRIOR FILING DATE: 2001-05-22  
 PRIOR APPLICATION NUMBER: 60/316,115  
 PRIOR FILING DATE: 2001-08-30  
 NUMBER OF SEQ ID NOS: 264  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO: 257  
 LENGTH: 8  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Beta-secretase Cleavage site  
 US-10-480-954-257

Qy	1 EVNLDAE 7.	1 EVNLDAE 7
Db		

RESULT 3  
 US-10-817-979-71  
 Sequence 71, Application US/10817979  
 Publication No. US20050196398A1  
 GENERAL INFORMATION:  
 APPLICANT: Gurney, et al  
 TITLE OF INVENTION: THEREOF  
 FILE REFERENCE: 2991540065  
 CURRENT APPLICATION NUMBER: US/10/817,979  
 CURRENT FILING DATE: 2004-04-05  
 PRIOR APPLICATION NUMBER: US 09/668,314  
 PRIOR FILING DATE: 2000-09-22  
 PRIOR APPLICATION NUMBER: US 60/169,232  
 PRIOR FILING DATE: 1999-12-06  
 PRIOR APPLICATION NUMBER: US 09/416,901  
 PRIOR FILING DATE: 1999-10-13  
 PRIOR APPLICATION NUMBER: US 60/155,493  
 PRIOR FILING DATE: 1999-09-23  
 PRIOR APPLICATION NUMBER: US 09/404,133  
 PRIOR FILING DATE: 1999-09-23  
 PRIOR APPLICATION NUMBER: PCT/US99/20881  
 PRIOR FILING DATE: 1999-09-23  
 PRIOR APPLICATION NUMBER: US 60/101,594  
 PRIOR FILING DATE: 1998-09-24  
 NUMBER OF SEQ ID NOS: 84  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 71  
 LENGTH: 8

TYPE: PRT  
 ORGANISM: Artificial sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic peptide  
 US-10-817-979-71

Query Match 100.0%; Score 34; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

RESULT 4  
 US-9-895-874-8  
 Sequence 8, Application US/09896874  
 Patent No. US2002016320A1  
 GENERAL INFORMATION:  
 APPLICANT: Fang, Lawrence Y.  
 APPLICANT: Frekos, John N.  
 APPLICANT: Gailunas, Andrea  
 APPLICANT: Hom, Roy  
 APPLICANT: Jagodzinska, Barbara

RESULT 5  
 US-09-896-874-8  
 Sequence 4, Application US/09896876  
 Publication No. US2002001403A1  
 GENERAL INFORMATION:  
 APPLICANT: Hom, Roy  
 APPLICANT: Mamo, Shumeye  
 APPLICANT: Tung, Jay  
 APPLICANT: Vagheese, Andrea  
 APPLICANT: Vargheese, John  
 APPLICANT: Fang, Larry  
 TITLE OF INVENTION: Methods to Treat Alzheimer's Disease  
 FILE REFERENCE: 01-1736-D  
 CURRENT APPLICATION NUMBER: US/09/816,876  
 CURRENT FILING DATE: 2001-03-23  
 PRIOR APPLICATION NUMBER: 60/191,528  
 PRIOR FILING DATE: 2000-03-23  
 NUMBER OF SEQ ID NOS: 5  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 4  
 LENGTH: 9

TYPE: PRT  
 ORGANISM: artificial sequence  
 FEATURE:  
 OTHER INFORMATION: synthetic peptide  
 US-09-816-876-4

Query Match 100.0%; Score 34; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

RESULT 6  
 US-09-896-139-8  
 Sequence 8, Application US/09896139  
 Patent No. US2002128355A1  
 GENERAL INFORMATION:  
 APPLICANT: Beck, James P.  
 APPLICANT: Fang, Lawrence Y.  
 APPLICANT: Frekos, John N.  
 APPLICANT: Gailunas, Andrea  
 APPLICANT: Hom, Roy  
 APPLICANT: Jagodzinska, Barbara

GenCore version 5.1.7  
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## OM protein - protein search, using sw model

Run on: March 15, 2006, 20:18:47 ; Search time 120 Seconds

(without alignments)  
24.373 Million cell updates/sec

Title: US-10-721-297-10

Perfect score: 34

Sequence: 1 EVNLDAE 7

Scoring table: BLOSUM2

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*

1: /cgn2\_6/prodata/1/pubseq/US07\_PUSCOMB.pep:\*

2: /cgn2\_6/prodata/1/pubseq/US08\_PUSCOMB.pep:\*

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4: /cgn2\_6/prodata/1/pubseq/US10\_PUSCOMB.pep:\*

5: /cgn2\_6/prodata/1/pubseq/US10B\_PUSCOMB.pep:\*

6: /cgn2\_6/prodata/1/pubseq/US11\_PUSCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Query Length DB ID Description

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1 34 100.0 7 5 US-10-726-967A-59 Sequence 59, Appl

2 34 100.0 8 5 US-10-480-954-257 Sequence 257, App

3 34 100.0 8 5 US-10-817-979-71 Sequence 71, Appl

4 34 100.0 9 3 US-09-895-874-8 Sequence 8, Appl

5 34 100.0 9 3 US-09-816-876-4 Sequence 8, Appl

6 34 100.0 9 3 US-09-896-139-8 Sequence 8, Appl

7 34 100.0 9 3 US-09-895-843-8 Sequence 8, Appl

8 34 100.0 9 3 US-09-908-943A-113 Sequence 8, Appl

9 34 100.0 9 3 US-09-895-871-8 Sequence 8, Appl

10 34 100.0 9 3 US-09-874-350A-209 Sequence 8, Appl

11 34 100.0 9 4 US-10-192-625-8 Sequence 8, Appl

12 34 100.0 9 4 US-10-192-424-8 Sequence 8, Appl

13 34 100.0 9 4 US-10-183-126A-8 Sequence 8, Appl

14 34 100.0 9 4 US-10-171-343-8 Sequence 8, Appl

15 34 100.0 9 4 US-10-264-707-8 Sequence 8, Appl

16 34 100.0 9 4 US-065-319-4 Sequence 8, Appl

17 34 100.0 9 4 US-10-337-075-8 Sequence 8, Appl

18 34 100.0 9 4 US-10-160-777-8 Sequence 8, Appl

19 34 100.0 9 4 US-10-192-543-8 Sequence 8, Appl

20 34 100.0 9 4 US-10-299-739-8 Sequence 8, Appl

21 34 100.0 9 4 US-10-685-698-107 Sequence 8, Appl

22 34 100.0 9 4 US-10-659-A-8 Sequence 8, Appl

23 34 100.0 9 5 US-10-801-487-113 Sequence 113, App

24 34 100.0 9 5 US-10-801-939-113 Sequence 113, App

25 34 100.0 9 5 US-10-801-509-113 Sequence 113, App

26 34 100.0 9 5 US-10-801-486-113 Sequence 113, App

27 34 100.0 9 5 US-10-621-311-1 Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-10-726-967A-59Sequence 59, Application US/10726967A  
Publication No. US20050074456A1

; GENERAL INFORMATION:

; TITLE OF INVENTION: Constructs for Homogenously Processed Preparations of Beta Site

; TITLE OF INVENTION: APP-CLEAVING ENZYME

; FILE REFERENCE: 2004345-0021

; CURRENT APPLICATION NUMBER: US/10/726, 967A

; CURRENT FILING DATE: 2003-12-02

; NUMBER OF SEQ ID NOS: 110

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 59

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Engineered BACB1 autoproteolysis site

US-10-726-967A-59

Query Match Best Local Similarity 100.0%; Score 34; DB 5; Length 7;

Matches 7; Conservativeness 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAE 7

Db 1 EVNLDAE 7

; APPLICANT: Brady, Stephen F.

; APPLICANT: Bruce, James E.

; APPLICANT: Chan-Dobson, Elizabeth

; APPLICANT: Garbky, Victor

; APPLICANT: Li, Yueming

; APPLICANT: Sardana, Mohinder

; APPLICANT: Shafer, Jules A.

; APPLICANT: Tang, Xiaoting

; TITLE OF INVENTION: BETA-SECRETASE SUBSTRATES AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 200861YP

; CURRENT APPLICATION NUMBER: US/10/480, 954

; CURRENT FILING DATE: 2003-11-21

; PRIOR APPLICATION NUMBER: PCT/US02/15590

; PRIORITY FILING DATE: 2002-05-17

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; APPLICANT: NEITZ, R. JEFFREY
; TITLE OF INVENTION: SUBSTITUTED UREA AND CARBAMATE, PHENACYL-2-HYDROXY-3-DIAMINOALKAN
; FILE REFERENCE: 09511.0005-00000
; CURRENT APPLICATION NUMBER: US/11/075,292
; CURRENT FILING DATE: 2005-03-09
; PRIORITY APPLICATION NUMBER: 60/622,589
; PRIORITY FILING DATE: 2004-10-28
; PRIORITY APPLICATION NUMBER: 60/591,857
; PRIORITY FILING DATE: 2004-07-29
; PRIORITY APPLICATION NUMBER: 60/575,829
; PRIORITY FILING DATE: 2004-06-02
; PRIORITY APPLICATION NUMBER: 60/551,192
; PRIORITY FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-075,292-10
Query Match          100.0%; Score 34; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0
Oy      1 EVNLDAE 7
Db      2 EVNLDAE 8
RESULT 3
US-11-090-520-8
Sequence 8, Application US/11090520
Publication No. US20050267199A1
GENERAL INFORMATION:
; APPLICANT: Hom, Roy
; APPLICANT: Tucker, John
; APPLICANT: John, Varghese
; APPLICANT: Shah, Neerav
TITLE OF INVENTION: 2-Amino- and 2-Thio- Substituted 1,3-Diaminopropanes
FILE REFERENCE: 04-244-A
CURRENT APPLICATION NUMBER: US/11/090,520
CURRENT FILING DATE: 2005-03-25
PRIORITY APPLICATION NUMBER: 60/555,461
PRIORITY FILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.3
SEQ ID NO 8
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE: OTHER INFORMATION: synthetic peptide
US-11-090-520-8
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Best Local Similarity 100.0%; Pred. No. 1.3e+05; Mismatches 0; Indels 0; Gaps 0;
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Db      2 EVNLDAE 8
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Sequence 8, Application US/11090520
Publication No. US20050267199A1
GENERAL INFORMATION:
; APPLICANT: JOHN, VARGHESE
; APPLICANT: HOM, ROY
; APPLICANT: SEALY, JENNIFER
; APPLICANT: AQUITO, JOSE
; APPLICANT: PROBST, GARY
; APPLICANT: TUNG, JAY
; APPLICANT: FANG, LAWRENCE
; TITLE OF INVENTION: METHODS OF TREATMENT OF AMYLOIDOSIS USING
; FILE REFERENCE: 09511.0004-00000
; CURRENT APPLICATION NUMBER: US/11/038,790
; CURRENT FILING DATE: 2005-01-21
; PRIORITY APPLICATION NUMBER: 60/619,948
; PRIORITY FILING DATE: 2004-10-20
; PRIORITY APPLICATION NUMBER: 60/591,908
; PRIORITY FILING DATE: 2004-07-29
; PRIORITY APPLICATION NUMBER: 60/619,947
; PRIORITY FILING DATE: 2004-10-20
; PRIORITY APPLICATION NUMBER: 60/591,858
; PRIORITY FILING DATE: 2004-10-20
; PRIORITY APPLICATION NUMBER: 60/591,885
; PRIORITY FILING DATE: 2004-07-29
; PRIORITY APPLICATION NUMBER: 60/591,908
; PRIORITY FILING DATE: 2004-07-29
; PRIORITY APPLICATION NUMBER: 60/591,858
; PRIORITY FILING DATE: 2004-06-02
; PRIORITY APPLICATION NUMBER: 60/575,798
; PRIORITY FILING DATE: 2004-06-02
; PRIORITY APPLICATION NUMBER: 60/575,799
; PRIORITY FILING DATE: 2004-06-02
; PRIORITY APPLICATION NUMBER: 60/537,551
; PRIORITY FILING DATE: 2004-01-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
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Sequence 10, Application US/11075445
Publication No. US20060014737A1
GENERAL INFORMATION:
; APPLICANT: JOHN, VARGHESE
; APPLICANT: HOM, ROY
; APPLICANT: SEALY, JENNIFER
; APPLICANT: TUCKER, JOHN
TITLE OF INVENTION: METHODS OF TREATMENT OF AMYLOIDOSIS USING BI-ARYL ASPARTYL PROTE
FILE REFERENCE: 09511.0006-00000
CURRENT APPLICATION NUMBER: US/11/075,445
; CURRENT FILING DATE: 2005-03-09
; PRIORITY APPLICATION NUMBER: 60/551,205
; PRIORITY FILING DATE: 2004-03-09
; PRIORITY APPLICATION NUMBER: 60/551,013
; PRIORITY FILING DATE: 2004-03-09
; PRIORITY APPLICATION NUMBER: 60/575,964
; PRIORITY FILING DATE: 2004-06-02

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RESULT 4

US-11-038-790-10

; Sequence 10, Application US/11038790

; Publication No. US20060014737A1

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GENERAL INFORMATION:

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GenCore version 5.1.7

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Title: US-10-721-297-10  
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Scoring table: BLOSUM62  
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Searched: 169630 seqs, 28622889 residues

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Post-processing: Minimum Match 0%  
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Database : Published Applications AA New:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	34	100.0	9	7 US-11-075-9210	Sequence 10, Appli
3	34	100.0	9	7 US-11-090-520-8	Sequence 8, Appli
4	34	100.0	9	7 US-11-038-790-10	Sequence 10, Appli
5	34	100.0	9	7 US-11-075-4510	Sequence 10, Appli
6	34	100.0	9	7 US-11-218-879-8	Sequence 8, Appli
7	34	100.0	10	6 US-10-895-861-2	Sequence 2, Appli
8	34	100.0	11	6 US-10-348-595-2	Sequence 5, Appli
9	34	100.0	11	6 US-10-348-595-4	Sequence 4, Appli
10	34	100.0	13	7 US-11-075-292-3	Sequence 3, Appli
11	34	100.0	13	7 US-11-090-520-1	Sequence 1, Appli
12	34	100.0	13	7 US-11-038-790-3	Sequence 3, Appli
13	34	100.0	13	7 US-11-075-445-3	Sequence 3, Appli
14	34	100.0	13	7 US-11-218-79-1	Sequence 1, Appli
15	34	100.0	23	6 US-10-348-595-7	Sequence 7, Appli
16	34	100.0	30	7 US-11-075-292-11	Sequence 11, Appli
17	34	100.0	30	7 US-11-090-520-9	Sequence 9, Appli
18	34	100.0	30	7 US-11-038-790-11	Sequence 11, Appli
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25	34	100.0	33	7 US-11-218-879-6	Sequence 6, Appli

#### ALIGNMENTS

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; Sequence 21, Application US/10895861
; Publication No. US20060019368A1
; GENERAL INFORMATION:
; APPLICANT: BALTINGER, Marcus L.
; TITLE OF INVENTION: CONSTRUCTS FOR HOMOGENOUSLY PROCESSED
; PREPARATIONS OF BETA SITE APP-CLEAVING ENZYME
; CURRENT APPLICATION NUMBER: US/10/895-, 861
; CURRENT FILING DATE: 2004-07-20
; PRIORITY APPLICATION NUMBER: US 60/430, 984
; PRIORITY FILING DATE: 2002-12-04
; PRIORITY APPLICATION NUMBER: PCT to be assigned
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapiens
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Query Match 100.0%; Score 34; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Sequence 1, Appli
Qy 1 EVNLDAE 7
Db 1 EVNLDAE 7
; APPLICANT: JOHN, VARGHESE
; APPLICANT: MAILLARD, MICHEL
; APPLICANT: TUCKER, JOHN
; APPLICANT: AQUINO, JOSE
; APPLICANT: HOM, ROY
; APPLICANT: TUNG, JAY
; APPLICANT: DRESSAN, DARREN
; APPLICANT: SHAH, NEERAV
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